

1/10

ATGGCTTTGG AACAGAACCA GTCAACAGAT TATTATTATG AGGAAAATGA	50
M A L E Q N Q S T D Y Y Y E E N E	
AATGAATGGC ACTTATGACT ACAGTCAATA TGAAGTATC TGTATCAAAG	100
M N G T Y D Y S Q Y E L I C I K E	
AAGATGTCAG AGAATTTGCA AAAGTTTTC TCCCTGTATT CCTCACAATA	150
D V R E F A K V F L P V F L T I	
GTTTTCGTCA TTGGACTTGC AGGCAATTCC ATGGTAGTGG CAATTTATGC	200
V F V I G L A G N S M V V A I Y A	
CTATTACAAG AAACAGAGAA CCAAACAGA TGTGTACATC CTGAATTTGG	250
Y Y K K Q R T K T D V Y I L N L A	
CTGTAGCAGA TTTACTCCTT CTATTCACTC TGCCTTTTTG GGCTGTTAAT	300
V A D L L L L F T L P F W A V N	
GCAGTTCATG GGTGGGTTTT AGGGAAAATA ATGTGCAAAA TAACTTCAGC	350
A V H G W V L G K I M C K I T S A	
CTTGATACACA CTAACTTTG TCTCTGGAAT GCAGTTTCTG GCTTGTATCA	400
L Y T L N F V S G M Q F L A C I S	
GCATAGACAG ATATGTGGCA GTAACATAAG TCCCCAGCCA ATCAGGAGTG	450
I D R Y V A V T K V P S Q S G V	
GGAAAACCAT GCTGGATCAT CTGTTTCTGT GTCTGGATGG CTGCCATCTT	500
G K P C W I I C F C V W M A A I L	
GCTGAGCATA CCCAGCTGG TTTTTTATAC AGTAAATGAC AATGCTAGGT	550
L S I P Q L V F Y T V N D N A R C	
GCATTCCCAT TTTCCCCCGC TACCTAGGAA CATCAATGAA AGCATTGATT	600
I P I F P R Y L G T S M K A L I	
CAAATGCTAG AGATCTGCAT TGGATTGTGA GTACCCTTTC TTATTATGGG	650
Q M L E I C I G F V V P F L I M G	
GGTGTGCTAC TTTATCACAG CAAGGACACT CATGAAGATG CCAAACATTA	700
V C Y F I T A R T L M K M P N I K	
AAATATCTCG ACCCTAAAA GTTCTGCTCA CAGTCGTTAT AGTTTTTCATT	750
I S R P L K V L L T V V I V F I	
GTCACCTAAC TGCCTTATAA CATTGTCAAG TTCTGCCGAG CCATAGACAT	800
V T Q L P Y N I V K F C R A I D I	
CATCTACTCC CTGATCACCA GCTGCAACAT GAGCAAACGC ATGGACATCG	850
I Y S L I T S C N M S K R M D I A	
CCATCCAAGT CACAGAAAGC ATCGCACTCT TTCACAGCTG CCTCAACCCA	900
I Q V T E S I A L F H S C L N P	
ATCCTTTATG TTTTATGAGG AGCATCTTTC AAAAAGTACG TTATGAAAGT	950
I L Y V F M G A S F K N Y V M K V	
GGCCAAGAAA TATGGGTCCT GGAGAAGACA GAGACAAAGT GTGGAGGAGT	1000
A K K Y G S W R R Q R Q S V E E F	
TTCCTTTTGA TTCTGAGGGT CCTACAGAGC CAACCAGTAC TTTTAGCATT	1050
P F D S E G P T E P T S T F S I	
TAAAGGTAAA ACTGCTCTGC CTTTGTCTTG GATACATATG AATGATGCTT	1100
- R - N C S A F C L D T Y E - C F	
TCCCCTCAAA TAAAACATCT GCCTTATTCT GAAAAAATAA AAAAAAM	1147
P L K - N I C L I L K K K K	

FIG. 1

CCX-CKR MALEQNQSTDY^YYE--ENEMNGT^Y-----DYSQYELI^QIK 33
 CCR9 MTPDTFTSPIPNMADD^YG-SESTSSM-ED^YVN----FNFTDF--YCEK
 CCR7 MDLGKPMKSVLVALLVIFQVCLCQDEVTD^YIGDNTTVDYTLFESLCSK
 CCR6 MSGESMNFSDVFDSS^YED^YFVS-----VNTS^YYS----VDSEML--LCSL
 STRL33 MAEH^YDYHED^YGFS-----SF-NDSSQEEHQDF--L---

TM1

CCX-CKR EDVREFAKVFLPVFLTIVFVIGLAGNSMVAI^YAYYKKQRTKTDV^YILNL 83
 CCR9 NNVRQFASHFLPPLYWL^YVFIVGALGNSL^YVLVY^YWYCTRVKITMTDMFILNL
 CCR7 KDVRNFKAWFLPIMYSIICFVGILGNGLVLT^YIY^YFKRLKIMTIT^YILNL
 CCR6 QEVRQFSRL^YFPIAYS^YLIC^YVFGLGNILV^YITFAFYKKARSMTDV^YILNM
 STRL33 ----QESKVFLPCMYLV^YVFVCGIVGNSL^YLVISIF^YYK^YLQSLTDVFLVNL

TM2

TM3

CCX-CKR AMADLL^YFLTL^YPFWA^YV-NAVHGV^YVLCKIMCKIT^YSAL^YTLNFVSGM^YQFLAC 132
 CCR9 A^YIADLL^YFLVTL^YPFWA^YIA-AADQWKFOT^YFMCKVVNSM^YYKMN^YFYSCVLLIMC
 CCR7 AVAD^YTL^YFLTL^YPFWAYS-AAKSWV^YFGVH^YFKLIFA^YYKMSFFSGMLLLLC
 CCR6 A^YIAD^YTL^YFLVTL^YPFWA^YVSHA^YTGA^YWVFSNATCKLLKGI^YYAIN^YFNCGMLLLTC
 STRL33 PLAD^YLVFVCTL^YPFWA^YYA-GIHEW^YVFGV^YCKSLLGI^YYTN^YFEYTSMLILTC

TM4

CCX-CKR ISIDRYVA^YVT^YK-VPSQSGVG^YKP---CWII^YCFVWMA^YAILLSI^YHQLVFYTV 178
 CCR9 ISVDRYIAIAQAMRAHTWREKRL^YLYSKMV^YFTI^YWLAAL^YCIHEILYSQI
 CCR7 ISIDRYVA^YIVQAVSAHRHRARVLLISKLS^YCVGSAILATVLSI^YHellySDL
 CCR6 ISMDRYIA^YIVQATKSFRLRSRTLPRTKII^YCLVV^YGLSVII^YSSSTFVFNQK
 STRL33 ITVD^YRFIVVVKATKAYNQQA^YKRMTWGKVTSL^YLIWISLLVSI^YEQIIYGNV

TM5

CCX-CKR NDNAR---CIPIFPRY-LGTSMKALIQMLEICIGFV^YVPFLIMGV^YCYFITA 224
 CCR9 KEESGIAIC^YTMVPS-DESTK^YLSAVLT^YLKVILGFFLPFVVMACCYTII
 CCR7 QRSSEQAMRCSLIT-EHVEAF-ITIQAQMVIG^YFLVPLLAMSF^YCYLVII
 CCR6 YNTQGS^YDVCEPKYQTVSEPIRW^YKLMLGL^YLELLFG^YFIPLMF^YMFICYTFIV
 STRL33 FNLDKL-IC^Y--GYH--DEAIS--TVVLATQMTL^YGFL^YPLLT^YTMIV^YCYSVII

TM6

CCX-CKR RTILMKMP^YNIKISRLK^YVLLT^YVIVFIVT^YQLPYN^YIVKFCRAIDIIYSLITS 274
 CCR9 HTLIQAKKSSKHKALKV^YTTIT^YVLTVFVLS^YQFPYNCILLVQ^YTIDAYAMFISN
 CCR7 RTLLQARN^YFERNKAI^YKVIIAVV^YVFIVF^YQLPYN^YGVLAQTVANFNITSST
 CCR6 KTLVQAQNSKRHKAI^YRMIIAV^YVLVFLAC^YQIPH^YMMVLLV-TAANLGKMNRS
 STRL33 KTL^YLHAGGFQK^YHRS^YLK^YLI^YFLVMAVELLTOM^YPFNL^YMKFIRSTH-----WE

FIG. 2A

TM7

CCX-CKR	CNMSKRMDTAIQVTESTALFHSCLNFIILYVFMGASFKNYVMK-----V	317
CCR9	CAVSTNIDICFQVTQTIAFFHSCLNFLVLYVFGERFRDLVKTLKNLGCI	
CCR7	CELSKQLNTAYDVTYSLACVRCCVNEFLYAFIGVKFRNDIFKLFKDLGCL	
CCR6	CQSEKLIGYTKTVTEVLAFHSCLNFLVLYAFIGQKFRNYFLKILKDLWCV	
STRL33	YYAMTSFHYTIMVTEATAYLRACLNEVLVYAFVSLKERKNFWKLVKDIGCL	

CCX-CKR	AKK--GSWRRQRQSVDEFPPDSEGP--TEPTSTFSI	350
CCR9	SQA-QWVSFTR----REGSLK-LSSMLLETTSGALSL	
CCR7	SQE-QLRWSS----CRHIRR-SSMSVEAETTTTFSP	
CCR6	RRKYKSSGFSCAGRYSENI SROTSETADNDNASSTFTM	
STRL33	P--Y--LGVSHQWKSEEDNSKTFSASHNVEATSMFQL	

FIG. 2A
(CONTINUED)

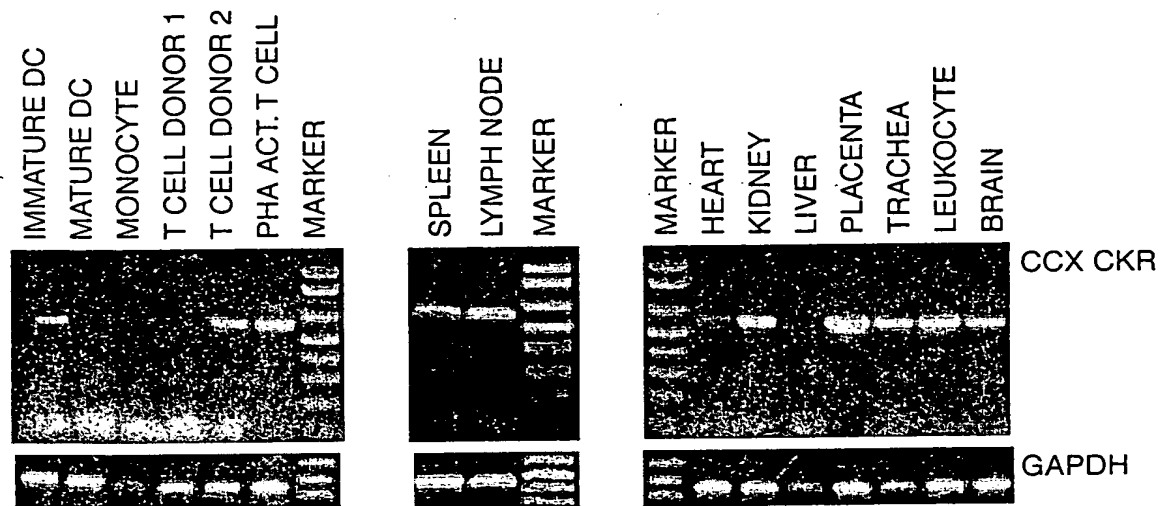


FIG. 2B

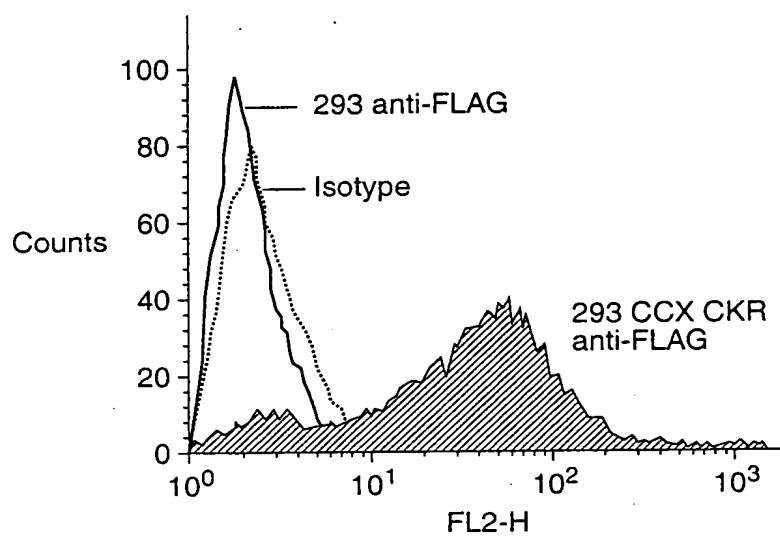


FIG. 2C

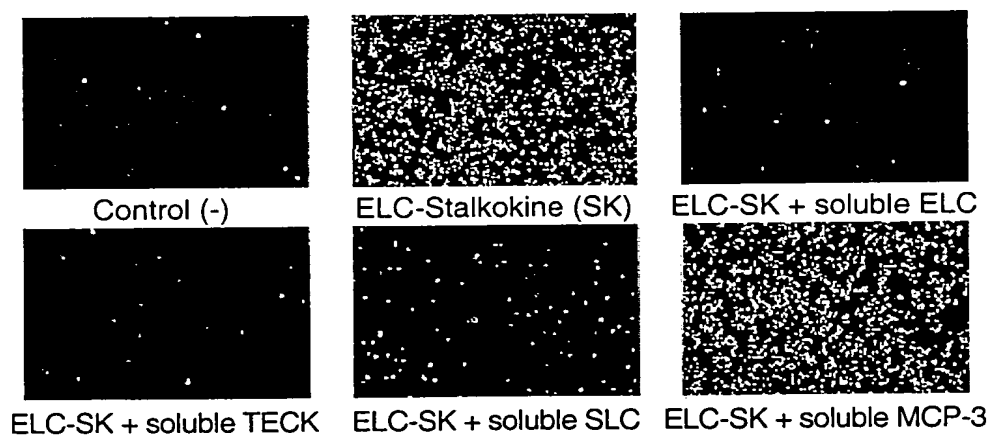


FIG. 3A

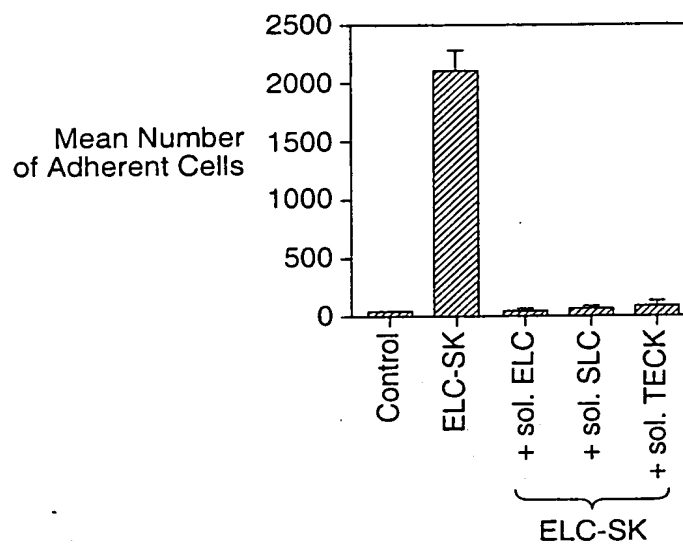


FIG. 3B

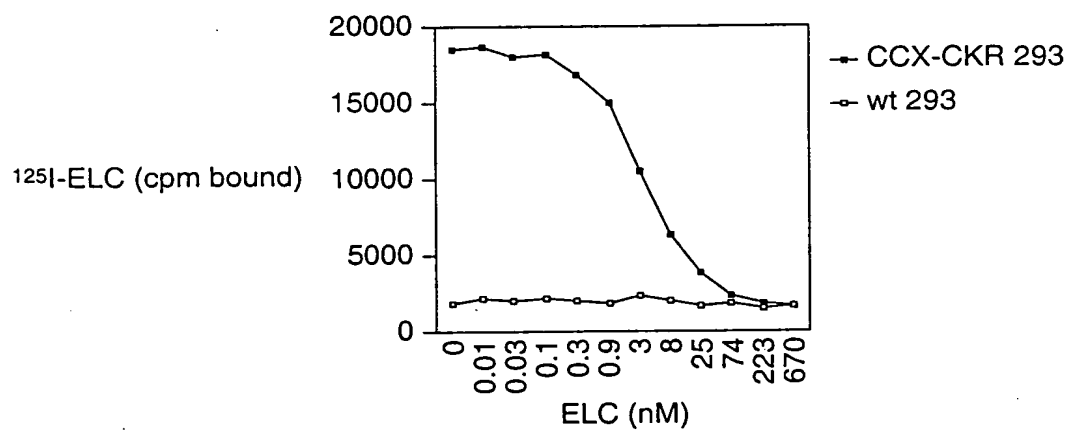


FIG. 3C

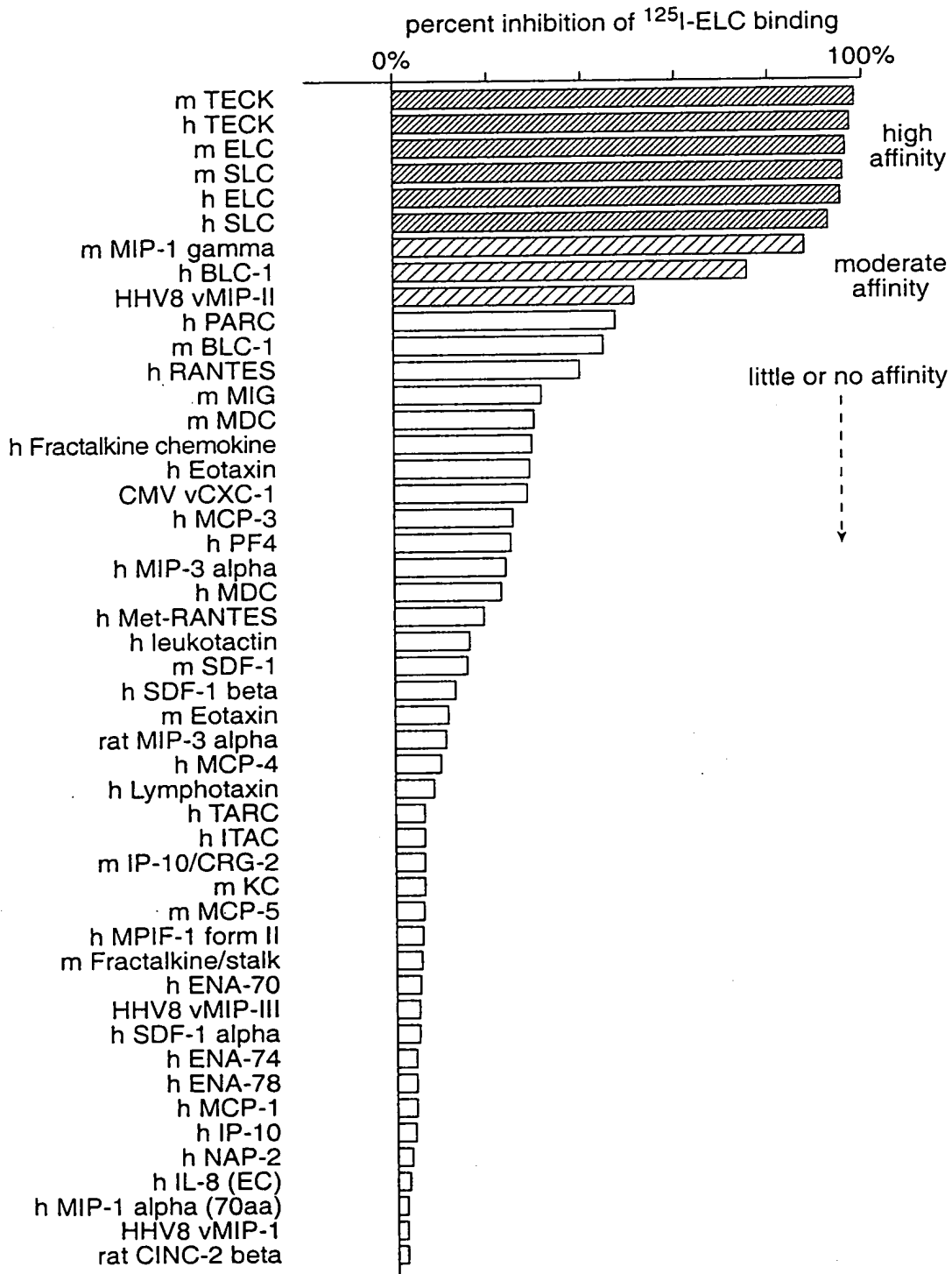


FIG. 4A

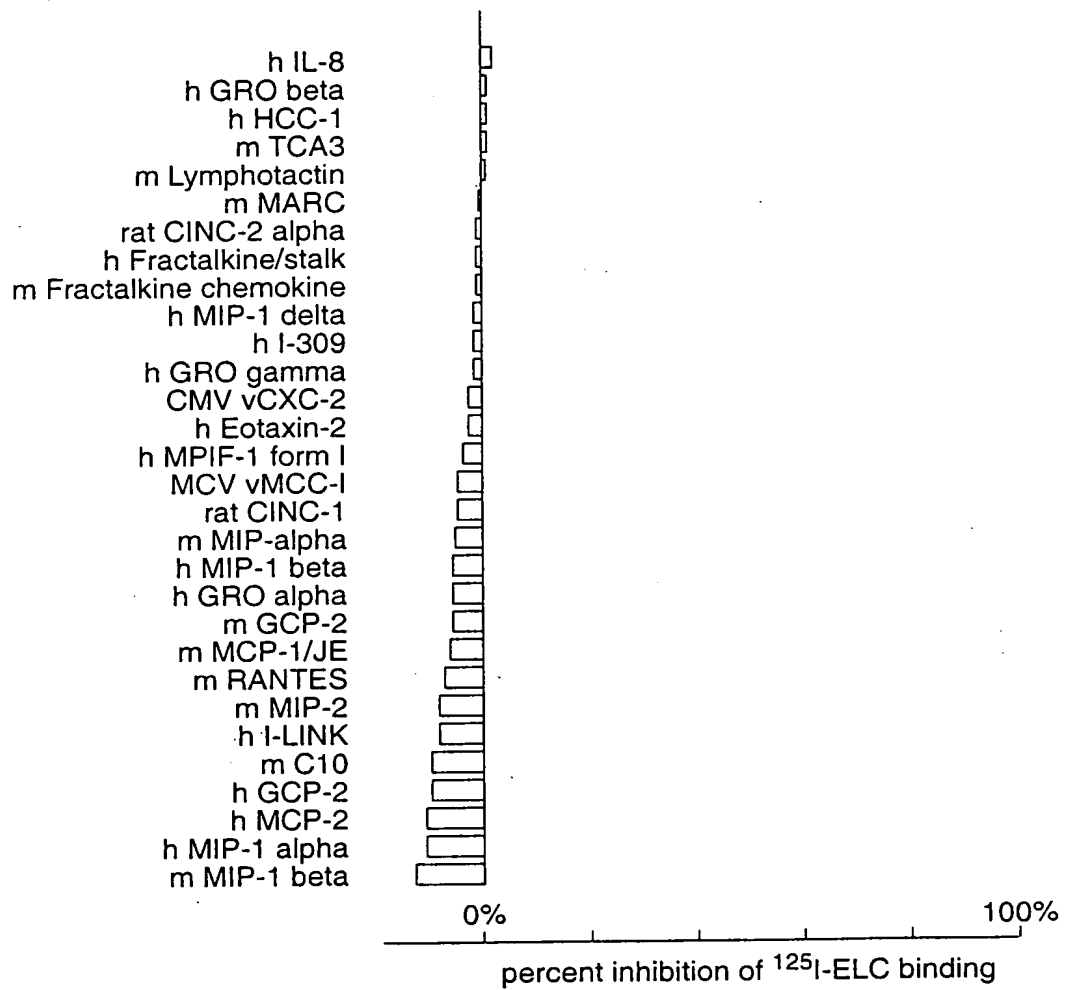
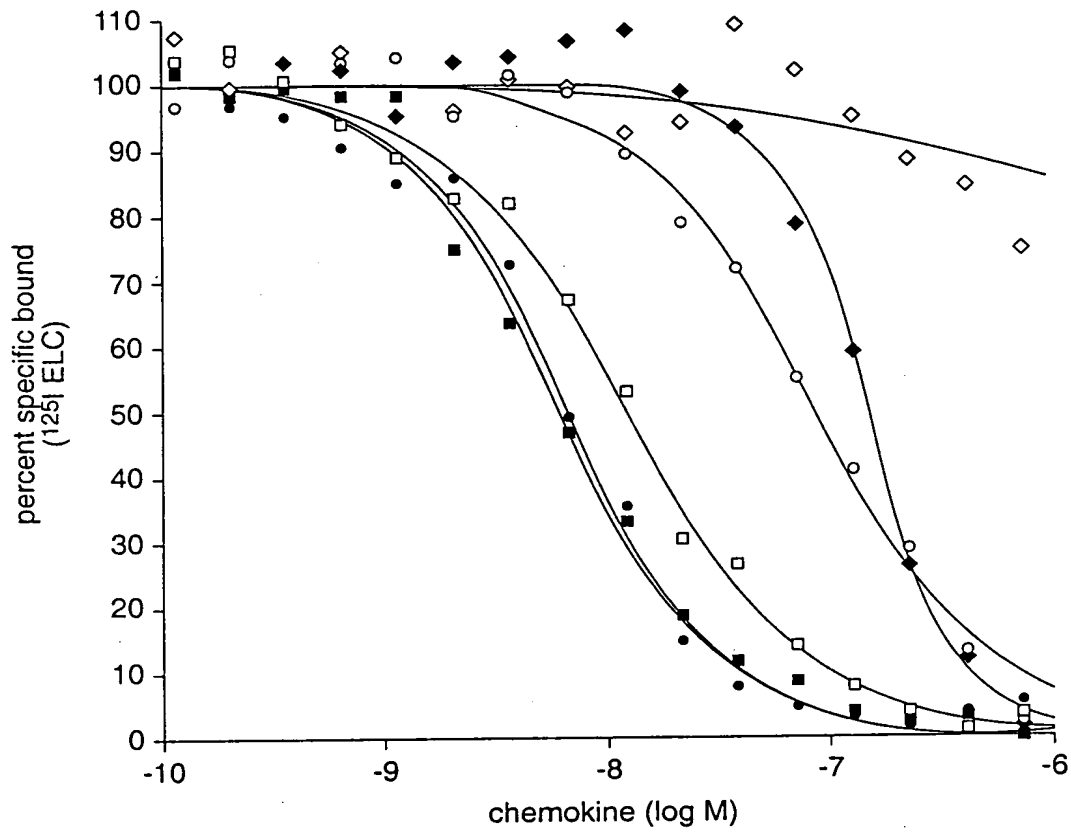


FIG. 4A
(CONTINUED)



human chemokines		murine chemokines	
■ h ELC	IC-50 6 nM	m ELC	IC-50 1 nM
□ h SLC	12 nM	m SLC	4 nM
● h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1 γ	70 nM
○ HHV8 vMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4B

5'upstream CCXCKR	ATGCAGCATC	TCGTTTATAA	AAGGCAACTA	GTGAAATTTA	GTGCAAATGC	50
5'upstream CCXCKR	TGAGAGAATT	TATTTAACTT	ATTTAAATTA	AATTTATATAA	TAACATCAAA	100
5'upstream CCXCKR	ATAAAAAATA	AATTTAATTT	AAATAAACCA	AGTAATTTGC	TATTTTCGTT	150
5'upstream CCXCKR	TTTATTCAAT	TTGTTGTAGA	TATACTTTTA	CGATTCACAA	AATTATGTAT	200
5'upstream CCXCKR	GTAAAGATTA	TAACACTATT	TATTCCTTTT	AGTTAAAATC	TAATTAAATT	250
5'upstream CCXCKR	TTCATATTTT	AAAAATCATT	TTTACATAAA	AGTCTTCACT	TTTATTTAGG	300
5'upstream CCXCKR	ATTTAATGAT	TAAGAAAATT	CTCCAGGGCA	TTATGTTTAT	TGTCCTGTTT	350
5'upstream CCXCKR	AAATCCAAGC	TCTTTCACAC	AGAATTGTAC	AAGCAAAGTT	TGAGTAACTA	400
5'upstream CCXCKR	ATCTTGGGGT	CATATTCCAA	TGTGGCTCCC	ATTAAAGCAT	TTCAAAGAGT	450
5'upstream CCXCKR	GCTAGATTCA	GGCTCACATA	TGTTACAGCA	ACAGGCTATA	CTCTAGGGAA	500
5'upstream CCXCKR	AGAACAAAAC	AGCTTGATAG	AAACTGTGTG	CTTTTAAGCA	TATTTAGACA	550
5'upstream CCXCKR	AATATCTATC	CTGTATTCTC	TTTGCCATCT	AGATTGGAGC	CATGGCTTTG ATGGCTTTG	600 9
5'upstream CCXCKR	GAACAGAACC	GTCAACAGA	TTATTATTAT	GAGGAGAGT	GAAATGAATG	649
5'upstream CCXCKR	GAACAGAACC	AGTCAACAGA	TTATTATTAT	GAGGA- AAAT	GAAATGAATG	58
5'upstream CCXCKR	GC-CTGATGA	CTACAGTCAG	TATGAACTGA	TCTGT-----	-----TC	685.
5'upstream CCXCKR	GCACTTATGA	CTACAGTCAA	TATGAACTGA	TCTGTATCAA	AGAAGATGTC	108
5'upstream CCXCKR	AGAGAAAGAGA	CAGAGGATAT	GC-ACAGGGT	TGCTCCCTGT	ATTGCTCACC	734
5'upstream CCXCKR	AGAGAA-----	-----TTT	GCAAAAGTTT	TCCTCCCTGT	ATTCTCACA	147
5'upstream CCXCKR	ATAG-----	-----	-----	-----AG	-----	740
5'upstream CCXCKR	ATAGTTTTCG	TCATTGGACT	TGCAGGCAAT	TCCATGGT-AG	TGGCAATTTA	197
5'upstream CCXCKR	-----	-----	-----	-----	-----	740
5'upstream CCXCKR	TGCCTATTAC	AAGAAACAGA	GAACCAAAAC	AGATGTGTAC	ATCCTGAATT	247
5'upstream CCXCKR	-----	-----	-----	-----	-----	740
5'upstream CCXCKR	TGGCTGTAGC	AGATTTACTC	CTTCTATTCA	CTCTGCCTTT	TTGGGCTGTT	297
5'upstream CCXCKR	-----	-----	-----	-----	-----	740
5'upstream CCXCKR	AATGCAGTTC	ATGGGTGGGT	TTTAGGGAAA	ATAATGTGCA	AAATAACTTC	347

FIG. 5

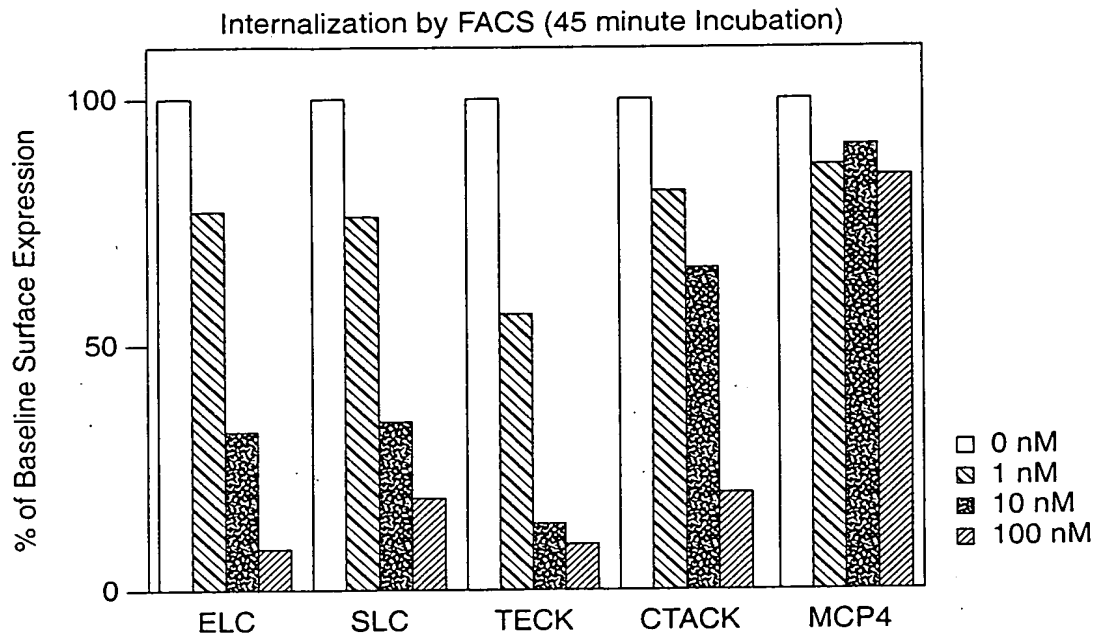


FIG. 6A

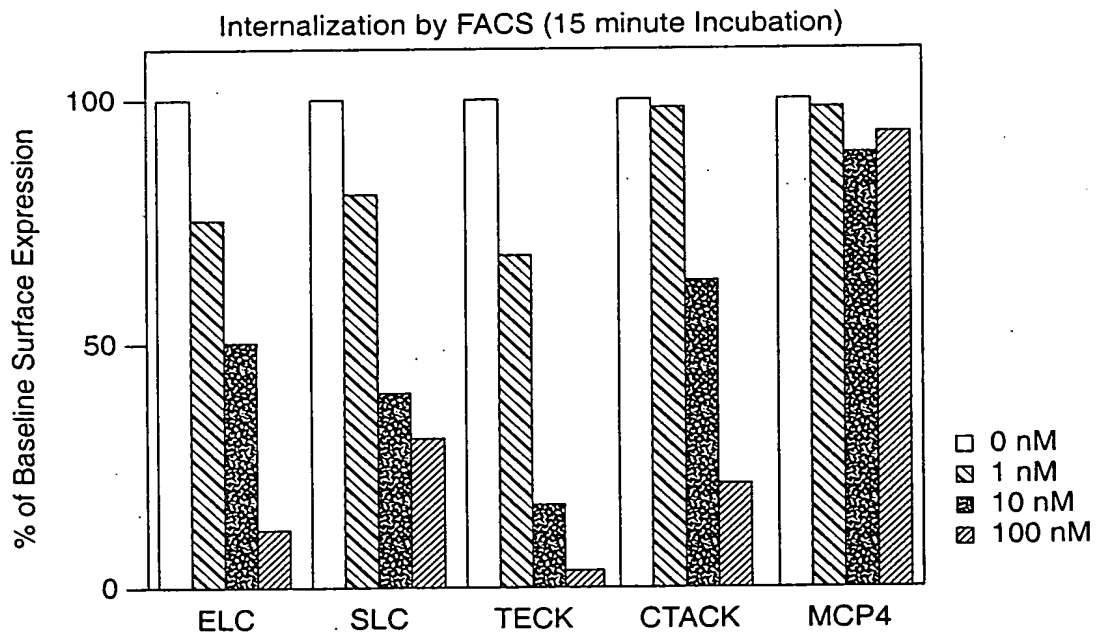


FIG. 6B